

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Zimmermann, Rainer; Park, John E.; Rettig, Wolfgang; Old, Lloyd J.
- (ii) TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN ALPHA, AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Felfe & Lynch
 - (B) STREET: 805 Third Avenue
 - (C) CITY: New York City
 - (D) STATE: New York
 - (E) COUNTRY: USA
 - (F) ZIP: 10022
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB storage
 - (B) COMPUTER: IBM PS/2
 - (C) OPERATING SYSTEM: PC-DOS
 - (D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/619,280
 - (B) FILING DATE: 18-MARCH-1996
 - (C) CLASSIFICATION: 435
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/230,491
 - (B) FILING DATE: 20-APRIL-1994
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Hanson, Norman D.
 - (B) REGISTRATION NUMBER: 30,946
 - (C) REFERENCE/DOCKET NUMBER: LUD 5330.1
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 688-9200
 - (B) TELEFAX: (212) 838-3884

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2815 Base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO: 1:

AAGAACGCC	CCAAAATCTG	TTTCTAATTT	TACAGAAATC	TTTGAAACT	TGGCACGGTA	60
TCAAAAGTC	CGTGGAAAGA	AAAAAACCTT	GTCCTGGCTT	CAGCTTCAA	CTACAAAGAC	120
AGACTTGGTC	CTTTCAACG	GTTCACAG	ATCCAGTGAC	CCACGCTCTG	AAGACAGAAT	180
TAGCTAACCT	TCAAAAACAT	CTGGAAAAAT	GAAGACTTGG	GTAAAAATCG	TATTTGGAGT	240
TGCCACCTCT	GCTGTGCTTG	CCTTATTGGT	GATGTGCATT	GTCTTACGCC	CTTCAAGAGT	300
TCATAACTCT	GAAGAAAATA	CAATGAGAGC	ACTCACACTG	AAGGATATTT	TAAATGGAAC	360
ATTTTCTTAT	AAAACATTTC	TTCCAAACTG	GATTCAGGA	CAAGAATATC	TTCATCAATC	420
TGAGATAAAC	AATATAGTAC	TTTATAATAT	TGAAACAGGA	CAATCATATA	CCATTTGAG	480
TAATAGAACCC	ATGAAAAGTG	TGAATGCTTC	AAATTACGGC	TTATCACCTG	ATCGGCAATT	540
TGATATATCTA	GAAAGTGATT	ATTCAAAGCT	TTGGAGATAC	TCTTACACAG	CAACATATTA	600
CATCTATGAC	CTTAGCAATG	GAGAATTGT	AAGAGGAAAT	GAGCTTCCCTC	GTCCAATTCA	660
GTATTTATGC	TGGTCGCCTG	TTGGGAGTAA	ATTAGCATAT	GTCTATCAA	ACAATATCTA	720
TTTGAAACAA	AGACCAGGAG	ATCCACCTTT	TCAAATAACA	TTTAATGGAA	GAGAAAATAA	780
AATATTTAAT	GGAATCCCAG	ACTGGGTTTA	TGAAGAGGAA	ATGCTTCCCA	CAAATATATGC	840
TCTCTGGTGG	TCTCTTAATG	AAAAATTTTT	GGCATATGCG	GAATTAAATG	ATAAGGATAT	900
ACCA GTT ATT	GCCTATTCCCT	ATTATGGCGA	TGAACAATAT	CCTAGAACAA	TAAATATTCC	960
ATACCCAAAG	GCTGGAGCTA	AGAATCCCGT	TGTTCGGATA	TTTATTATCG	ATACCACCTA	1020
CCCTGCGTAT	GTAGGTCCCC	AGGAAGTGCC	TGTTCCAGCA	ATGATAGCCT	CAAGTGATTA	1080
TTATTCAGT	TGGCTCACGT	GGGTTACTGA	TGAACGAGTA	TGTTTGCGAGT	GGCTAAAAG	1140
AGTCCAGAAT	GTTTGGTCC	TGTCTATATG	TGACTTCAGG	GAAGACTGGC	AGACATGGGA	1200
TTGTCCAAAG	ACCCAGGAGC	ATATAGAAGA	AAGCAGAACT	GGATGGGCTG	GTGGATTCTT	1260
TGTTTCAAGA	CCAGTTTCA	GCTATGATGC	CATTCGTAC	TACAAAATAT	TTAGTGACAA	1320
GGATGGCTAC	AAACATATTC	ACTATATCAA	AGACACTGTG	AAAAATGCTA	TTCAAATTAC	1380
AAGTGGCAAG	TGGGAGGCCA	TAAATATATT	CAGAGTAACA	CAGGATTTCAC	TGTTTTATTC	1440
TAGCAATGAA	TTGAAGAAT	ACCCCTGAAAG	AAGAAACATC	TACAGAATTA	GCATTGGAAG	1500
CTATCCTCCA	AGCAAGAAGT	GTGTTACTTG	CCATCTAAGG	AAAGAAAGGT	GCCAATATTA	1560
CACAGCAAGT	TTCAGCGACT	ACGCCAAGTA	CTATGCACTT	GTCTGCTACG	GCCCAGGCAT	1620
CCCCATTTC	ACCCCTTCATG	ATGGACGCAC	TGATCAAGAA	ATTAAAATCC	TGGAAGAAAA	1680
CAAGGAATTG	GAAAATGCTT	TGAAAAATAT	CCAGCTGCCT	AAAGAGGAAA	TTAAGAAACT	1740
TGAAGTAGAT	GAAATTACTT	TATGGTACAA	GATGATTCTT	CCTCCTCAAT	TTGACAGATC	1800
AAAGAAGTAT	CCCTGCTAA	TTCAAGTGT	TGGTGGTCCC	TGCAGTCAGA	GTGTAAGGTC	1860
TGTATTTGCT	GTTAATTGGA	TATCTTATCT	TGCAAGTAAG	GAAGGGATGG	TCATTGCCTT	1920
GGTGGATGGT	CGAGGAACAG	CTTCCAAGG	TGACAAACTC	CTCTATGCAG	TGTATCGAAA	1980
GCTGGGTGTT	TATGAAGTTG	AAGACCAGAT	TACAGCTGTC	AGAAAATTCA	TAGAAATGGG	2040
TTTCATTGAT	GAAAAAAAGAA	TAGCCATATG	GGGCTGGTCC	TATGGAGGAT	ACGTTTCATC	2100
ACTGGCCCTT	GCATCTGGAA	CTGGTCTTT	CAAATGTGGT	ATAGCAGTGG	CTCCAGTCTC	2160
CAGCTGGGAA	TATTACGCGT	CTGTCTACAC	AGAGAGATT	ATGGGCTCTCC	CAACAAAGGA	2220
TGATAATCTT	GAGCACTATA	AGAATTCAAC	TGTGATGGCA	AGAGCAGAAT	ATTTCAGAAA	2280
TGTAGACTAT	CTTCTCATCC	ACGGAACAGC	AGATGATAAT	GTGCACTTTC	AAAACTCAGC	2340
ACAGATTGCT	AAAGCTCTGG	TTAATGCACA	AGTGGATTTC	CAGGCAATGT	GGTACTCTGA	2400
CCAGAACAC	GGCTTATCCG	GCCTGTCCAC	GAACCACTTA	TACACCCACA	TGACCCACTT	2460
CCTAAAGCAG	TGTTTCTCTT	TGTCAAGACTA	AAAACGATGC	AGATGCAAGC	CTGTATCAGA	2520
ATCTGAAAAC	CTTATATAAA	CCCCTCAGAC	AGTTTGCTTA	TTTTATTCTT	TATGTTGTAA	2580
AATGCTAGTA	TAAACAAACA	AATTAATGTT	GTTCTAAAGG	CTGTTAAAAAA	AAAGATGAGG	2640
ACTCAGAACT	TCAAGCTAAA	TATTGTTAC	ATTTTCTGGT	ACTCTGTGAA	AGAAGAGAAA	2700

AGGGAGTCAT GCATTTGCT TTGGACACAG TGTTTATCA CCTGTTCATT TGAAGAAAAA 2760
TAATAAAGTC AGAAGTTCAA AAAAAAAA AAAAAAAA AAAGCGGCCG CTCGA 2815

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Lys Thr Trp Val Lys Ile Val Phe Gly Val Ala Thr Ser Ala Val
5 10 15

Leu Ala Leu Leu Val Met Cys Ile Val Leu Arg Pro Ser Arg Val His
20 25 30

Asn Ser Glu Glu Asn Thr Met Arg Ala Leu Thr Leu Lys Asp Ile Leu
35 40 45

Asn Gly Thr Phe Ser Tyr Lys Thr Phe Phe Pro Asn Trp Ile Ser Gly
50 55 60

Gln Glu Tyr Leu His Gln Ser Ala Asp Asn Asn Ile Val Leu Tyr Asn
65 70 75 80

Ile Glu Thr Gly Gln Ser Tyr Thr Ile Leu Ser Asn Arg Thr Met Lys
85 90 95

Ser Val Asn Ala Ser Asn Tyr Gly Leu Ser Pro Asp Arg Gln Phe Val
100 105 110

Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp Arg Tyr Ser Tyr Thr Ala
115 120 125

Thr Tyr Tyr Ile Tyr Asp Leu Ser Asn Gly Glu Phe Val Arg Gly Asn
130 135 140

Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys Trp Ser Pro Val Gly Ser
145 150 155 160

Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile Tyr Leu Lys Gln Arg Pro
165 170 175

Gly Asp Pro Pro Phe Gln Ile Thr Phe Asn Gly Arg Glu Asn Lys Ile
180 185 190

Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu Glu Glu Met Leu Pro Thr
195 200 205

Lys Tyr Ala Leu Trp Trp Ser Pro Asn Gly Lys Phe Leu Ala Tyr Ala
210 215 220

Glu Phe Asn Asp Lys Asp Ile Pro Val Ile Ala Tyr Ser Tyr Tyr Gly
225 230 235 240

Asp Glu Gln Tyr Pro Arg Thr Ile Asn Ile Pro Tyr Pro Lys Ala Gly
245 250 255

Ala Lys Asn Pro Val Val Arg Ile Phe Ile Ile Asp Thr Thr Tyr Pro
260 265 270

Ala Tyr Val Gly Pro Gln Glu Val Pro Val Pro Ala Met Ile Ala Ser
275 280 285

Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp Val Thr Asp Glu Arg Val
290 295 300

Cys Leu Gln Trp Leu Lys Arg Val Gln Asn Val Ser Val Leu Ser Ile
305 310 315 320

Cys Asp Phe Arg Glu Asp Trp Gln Thr Trp Asp Cys Pro Lys Thr Gln
325 330 335

Glu His Ile Glu Glu Ser Arg Thr Gly Trp Ala Gly Gly Phe Phe Val
340 345 350

Ser Arg Pro Val Phe Ser Tyr Asp Ala Ile Ser Tyr Tyr Lys Ile Phe
355 360 365

Ser Asp Lys Asp Gly Tyr Lys His Ile His Tyr Ile Lys Asp Thr Val
370 375 380

Glu Asn Ala Ile Gln Ile Thr Ser Gly Lys Trp Glu Ala Ile Asn Ile
385 390 395 400

Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr Ser Ser Asn Glu Phe Glu
405 410 415

Glu Tyr Pro Gly Arg Arg Asn Ile Tyr Arg Ile Ser Ile Gly Ser Tyr
420 425 430

Pro Pro Ser Lys Lys Cys Val Thr Cys His Leu Arg Lys Glu Arg Cys
435 440 445

Gln Tyr Tyr Thr Ala Ser Phe Ser Asp Tyr Ala Lys Tyr Tyr Ala Leu
450 455 460

Val Cys Tyr Gly Pro Gly Ile Pro Ile Ser Thr Leu His Asp Gly Arg
465 470 475 480

Thr Asp Gln Glu Ile Lys Ile Leu Glu Glu Asn Lys Glu Leu Glu Asn
485 490 495

Ala Leu Lys Asn Ile Gln Leu Pro Lys Glu Glu Ile Lys Lys Leu Glu
500 505 510

Val Asp Glu Ile Thr Leu Trp Tyr Lys Met Ile Leu Pro Pro Gln Phe
515 520 525

Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile Gln Val Tyr Gly Gly Pro
530 535 540

Cys Ser Gln Ser Val Arg Ser Val Phe Ala Val Asn Trp Ile Ser Tyr
545 550 555 560

Leu Ala Ser Lys Glu Gly Met Val Ile Ala Leu Val Asp Gly Arg Gly -
565 570 575

Thr Ala Phe Gln Gly Asp Lys Leu Leu Tyr Ala Val Tyr Arg Lys Leu
580 585 590

Gly Val Tyr Glu Val Glu Asp Gln Ile Thr Ala Val Arg Lys Phe Ile
595 600 605

Glu Met Gly Phe Ile Asp Glu Lys Arg Ile Ala Ile Trp Gly Trp Ser
610 615 620

Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu Ala Ser Gly Thr Gly Leu
625 630 635 640

Phe Lys Cys Gly Ile Ala Val Ala Pro Val Ser Ser Trp Glu Tyr Tyr
645 650 655

Ala Ser Val Tyr Thr Glu Arg Phe Met Gly Leu Pro Thr Lys Asp Asp
660 665 670

Asn Leu Glu His Tyr Lys Asn Ser Thr Val Met Ala Arg Ala Glu Tyr
675 680 685

Phe Arg Asn Val Asp Tyr Leu Leu Ile His Gly Thr Ala Asp Asp Asn
690 695 700

Val His Phe Gln Asn Ser Ala Gln Ile Ala Lys Ala Leu Val Asn Ala
705 710 715 720

Gln Val Asp Phe Gln Ala Met Trp Tyr Ser Asp Gln Asn His Gly Leu
725 730 735

Ser Gly Leu Ser Thr Asn His Leu Tyr Thr His Met Thr His Phe Leu
740 745 750

Lys Gln Cys Phe Ser Leu Ser Asp
755 760

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Lys Thr Pro Trp Lys Val Leu Leu Gly Leu Leu Gly Ala Ala Ala .
5 10 15

Leu Val Thr Ile Ile Thr Val Pro Val Val Leu Leu Asn Lys Gly Thr
20 25 30

Asp Asp Ala Thr Ala Asp Ser Arg Lys Thr Tyr Thr Leu Thr Asp Tyr
35 40 45

Leu Lys Asn Thr Tyr Arg Leu Lys Leu Tyr Ser Leu Arg Trp Ile Ser
50 55 60

Asp His Glu Tyr Leu Tyr Lys Gln Glu Asn Asn Ile Leu Val Phe Asn
65 70 75 80

Ala Glu Tyr Gly Asn Ser Ser Val Phe Leu Glu Asn Ser Thr Phe Asp
85 90 95

Glu Phe Gly His Ser Ile Asn Asp Tyr Ser Ile Ser Pro Asp Gly Gln
100 105 110

Phe Ile Leu Leu Glu Tyr Asn Tyr Val Lys Gln Trp Arg His Ser Tyr
115 120 125

Thr Ala Ser Tyr Asp Ile Tyr Asp Leu Asn Lys Arg Gln Leu Ile Thr
130 135 140

Glu Glu Arg Ile Pro Asn Asn Thr Gln Trp Val Thr Trp Ser Pro Val
145 150 155 165

Gly His Lys Leu Ala Tyr Val Trp Asn Asn Asp Ile Tyr Val Lys Ile
170 175 180

Glu Pro Asn Leu Pro Ser Tyr Arg Ile Thr Trp Thr Gly Lys Glu Asp
185 190 195

Ile Ile Tyr Asn Gly Ile Thr Asp Trp Val Tyr Glu Glu Val Phe
200 205 210

Ser Ala Tyr Ser Ala Leu Trp Trp Ser Pro Asn Gly Thr Phe Leu Ala
215 220 225

Tyr Ala Gln Phe Asn Asp Thr Glu Val Pro Leu Ile Glu Tyr Ser Phe
230 235 240 245

Tyr Ser Asp Glu Ser Leu Gln Tyr Pro Lys Thr Val Arg Val Pro Tyr
250 255 260

Pro Lys Ala Gly Ala Val Asn Pro Thr Val Lys Phe Phe Val Val Asn
265 270 275

Thr Asp Ser Leu Ser Ser Val Thr Asn Ala Thr Ser Ile Gln Ile Thr
280 285 290

Ala Pro Ala Ser Met Leu Ile Gly Asp His Tyr Leu Cys Asp Val Thr
295 300 305

Trp Ala Thr Gln Glu Arg Ile Ser Leu Gln Trp Leu Arg Arg Ile Gln
310 315 320 325

Asn Tyr Ser Val Met Asp Ile Cys Asp Tyr Asp Glu Ser Ser Gly Arg
330 335 340

Trp Asn Cys Leu Val Ala Arg Gln His Ile Glu Met Ser Thr Thr Gly
345 350 355

Trp Val Gly Arg Phe Arg Pro Ser Glu Pro His Phe Thr Leu Asp Gly
360 365 370

Asn Ser Phe Tyr Lys Ile Ile Ser Asn Glu Glu Gly Tyr Arg His Ile
375 380 385

Cys Tyr Phe Gln Ile Asp Lys Lys Asp Cys Thr Phe Ile Thr Lys Gly
390 395 400 405

Thr Trp Glu Val Ile Gly Ile Glu Ala Leu Thr Ser Asp Tyr Leu Tyr
410 415 420

Tyr Ile Ser Asn Glu Tyr Lys Gly Met Pro Gly Gly Arg Asn Leu Tyr
425 430 435

Lys Ile Gln Leu Ser Asp Tyr Thr Lys Val Thr Cys Leu Ser Cys Glu
440 445 450

Leu Asn Pro Glu Arg Cys Gln Tyr Tyr Ser Val Ser Phe Ser Lys Glu
455 460 460

Ala Lys Tyr Tyr Gln Leu Arg Cys Ser Gly Pro Gly Leu Pro Leu Tyr
465 470 475 480

Thr Leu His Ser Ser Val Asn Asp Lys Gly Leu Arg Val Leu Glu Asp
485 490 495

Asn Ser Ala Leu Asp Lys Met Leu Gln Asn Val Gln Met Pro Ser Lys
500 505 510

Lys Leu Asp Phe Ile Ile Leu Asn Glu Thr Lys Phe Trp Tyr Gln Met
515 520 525

Ile Leu Pro Pro His Phe Asp Lys Ser Lys Lys Tyr Pro Leu Leu Leu
530 535 540

Asp Val Tyr Ala Gly Pro Cys Ser Gln Lys Ala Asp Thr Val Phe Arg
545 550 555 560

Leu Asn Trp Ala Thr Tyr Leu Ala Ser Thr Glu Asn Ile Ile Val Ala
565 570 575

Ser Phe Asp Gly Arg Gly Ser Gly Tyr Gln Gly Asp Lys Ile Met His
580 585 590

Ala Ile Asn Arg Arg Leu Gly Thr Phe Glu Val Glu Asp Gln Ile Glu
595 600 605

Ala Ala Arg Gln Phe Ser Lys Met Gly Phe Val Asp Asn Lys Arg Ile
610 615 620

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Thr Ser Met Val Leu
625 630 635 640

Gly Ser Gly Ser Gly Val Phe Lys Cys Gly Ile Ala Val Ala Pro Val
645 650 655

Ser Arg Trp Glu Tyr Tyr Asp Ser Val Tyr Thr Glu Arg Tyr Met Gly
660 665 670

Leu Pro Thr Pro Glu Asp Asn Leu Asp His Tyr Arg Asn Ser Thr Val
675 680 685

Met Ser Arg Ala Glu Asn Phe Lys Gln Val Glu Tyr Leu Leu Ile His
690 695 700

Gly Thr Ala Asp Asp Asn Val His Phe Gln Gln Ser Ala Gln Ile Ser
705 710 715 720

Lys Ala Leu Val Asp Val Gly Val Asp Phe Gln Ala Met Trp Tyr Thr
725 730 735

Asp Glu Asp His Gly Ile Ala Ser Ser Thr Ala His Gln His Ile Tyr
740 745 750

Thr His Met Ser His Phe Ile Lys Gln Cys Phe Ser Leu Pro
755 760 765

- (2) INFORMATION FOR SEQ ID NO: 4:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ix) FEATURE:
- (D) OTHER INFORMATION: The first Xaa is either Trp or Phe.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Xaa Gly Trp Ser Tyr Gly Gly
5

- (2) INFORMATION FOR SEQ ID NO: 5:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Phe Gly Lys Asp Tyr Gly Gly
5

- (2) INFORMATION FOR SEQ ID NO: 6:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ix) FEATURE:
- (D) OTHER INFORMATION: Xaa is either Ala or Gly
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Gly Thr Xaa Asp Asp Asn Val
5

- (2) INFORMATION FOR SEQ ID NO: 7:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Ala Gln Asn His Gly Leu Ser
5

- (2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION:

The first Xaa is Glu or Ser. When the first Xaa is Glu, the second Xaa is Gly and the third is Ala. When the first Xaa is Ser, the second Xaa is Ser, and the third Xaa is Arg.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Asp Xaa Asp His Xaa Ile Xaa

5

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION:

Xaa is Pro or Ala.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Xaa Thr Ala Asp Glu Lys Ile

5

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION:

Xaa is Thr, His or Ser.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Asp Glu Ser His Tyr Phe Xaa

5